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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,438

DATE: 09/16/2002

TIME: 15:21:40

Input Set : N:\Crf3\RULE60\10005438.raw

Output Set: N:\CRF4\09162002\J005438.raw

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1 <110> APPLICANT: Tse Wen Chang
2   Liming Yu
3 <120> TITLE OF INVENTION: Hybrid with Interferon-alpha and an
4   Immunoglobulin Fc for Treatment of Tumors
5 <130> FILE REFERENCE: 95-2AAA
7 <140> CURRENT APPLICATION NUMBER: 10/005,438
8 <141> CURRENT FILING DATE: 2001-12-03
10 <150> PRIOR APPLICATION NUMBER: US/09/268,787
11 <151> PRIOR FILING DATE: 1999-03-16
14 <150> PRIOR APPLICATION NUMBER: 08/994,719
15 <151> PRIOR FILING DATE: 1997-12-19
16 <150> PRIOR APPLICATION NUMBER: 08/719,331
17 <151> PRIOR FILING DATE: 1996-09-25
18 <150> PRIOR APPLICATION NUMBER: 08/579,211
19 <151> PRIOR FILING DATE: 1995-12-28
20 <160> NUMBER OF SEQ ID NOS: 11
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1254
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)...(1251)
30 <223> OTHER INFORMATION: recombinant sequence based on human sequences
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32   atg gcc ttg acc ttt gct tta ctg gtg gcc ctc ctg gtg ctc agc tgc      48
33   Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
34   1           5           10           15
35   aag tca agc tgc tct ctg ggc tgt gat ctg cct caa acc cac agc ctg      96
36   Lys Ser Ser Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu
37   20           25           30
38   ggt agc agg agg acc ttg atg ctc ctg gca cag atg agg aaa atc tct      144
39   Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Lys Ile Ser
40   35           40           45
41   ctt ttc tcc tgc ttg aag gac aga cat gac ttt gga ttt ccc cag gag      192
42   Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
43   50           55           60
44   gag ttt ggc aac cag ttc caa aag gct gaa acc atc cct gtc ctc cat      240
45   Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
46   65           70           75           80
47   gag atg atc cag cag atc ttc aat ctc ttc agc aca aag gac tca tct      288
48   Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser

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49					85				90				95				
50	gct	gct	tg	gat	gag	acc	ctc	cta	gac	aaa	ttc	tac	act	gaa	ctc	tac	336
51	Ala	Ala	Trp	Asp	Glu	Thr	Leu	Leu	Asp	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	
52					100				105				110				
53	cag	cag	ctg	aat	gac	ctg	gaa	gcc	tgt	gtg	ata	cag	ggg	gtg	ggg	gtg	384
54	Gln	Gln	Leu	Asn	Asp	Leu	Glu	Ala	Cys	Val	Ile	Gln	Gly	Val	Gly	Val	
55				115				120					125				
56	aca	gag	act	ccc	ctg	atg	aag	gag	gac	tcc	att	ctg	gct	gtg	agg	aaa	432
57	Thr	Glu	Thr	Pro	Leu	Met	Lys	Glu	Asp	Ser	Ile	Leu	Ala	Val	Arg	Lys	
58		130					135					140					
59	tac	ttc	caa	aga	atc	act	ctc	tat	ctg	aaa	gag	aag	aaa	tac	agc	cct	480
60	Tyr	Phe	Gln	Arg	Ile	Thr	Leu	Tyr	Leu	Lys	Glu	Lys	Lys	Tyr	Ser	Pro	
61	145				150				155						160		
62	tgt	gcc	tg	gag	gtt	gtc	aga	gca	gaa	atc	atg	aga	tct	ttt	tct	ttg	528
63	Cys	Ala	Trp	Glu	Val	Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Leu	
64				165				170					175				
65	tca	aca	aac	ttg	caa	gaa	agt	tta	aga	agt	aag	gaa	gag	tcc	aaa	tat	576
66	Ser	Thr	Asn	Leu	Gln	Glu	Ser	Leu	Arg	Ser	Lys	Glu	Glu	Ser	Lys	Tyr	
67			180					185				190					
68	ggg	ccc	ccg	tgc	cca	tca	tgc	cca	gca	cct	gag	ttc	ctg	ggg	gga	cca	624
69	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	
70			195					200				205					
71	tca	gtc	ttc	ctg	ttc	ccc	cca	aaa	ccc	aag	gac	act	ctc	atg	atc	tcc	672
72	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
73		210					215					220					
74	cgg	acc	cct	gag	gtc	acg	tgc	gtg	gtg	gtg	gac	gtg	agc	cag	gaa	gac	720
75	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	
76	225				230				235						240		
77	ccc	gag	gtc	cag	ttc	aac	tg	tac	gtg	gat	ggc	gtg	gag	gtg	cat	aat	768
78	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
79			245					250				255					
80	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	ttc	aac	agc	acg	tac	cgt	gtg	816
81	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	
82			260					265				270					
83	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tg	ctg	aac	ggc	aag	gag	864
84	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
85			275					280				285					
86	tac	aag	tgc	aag	gtc	tcc	aac	aaa	ggc	ctc	ccg	tcc	tcc	atc	gag	aaa	912
87	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	
88		290					295				300						
89	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gag	cca	cag	gtg	tac	acc	960
90	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	
91	305				310				315						320		
92	ctg	ccc	cca	tcc	cag	gag	gag	atg	acc	aag	aac	cag	gtc	agc	ctg	acc	1008
93	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	
94			325					330				335					
95	tgc	ctg	gtc	aaa	ggc	ttc	tac	ccc	agc	gac	atc	gcc	gtg	gag	tg	gag	1056
96	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	
97			340					345				350					

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98      agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg      1104
99      Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
100             355             360             365
101      gac tcc gac ggc tcc ttc ttc ctc tac agc agg ctg acc gtg gac aag      1152
102      Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
103             370             375             380
104      agc agg tgg cag gag ggg aat gtc ttc tca tgc tcc gtg atg cat gag      1200
105      Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
106      385             390             395             400
107      gct ctg cac aac cac tac aca cag aag agc ctc tcc ctg tct ctg ggt      1248
108      Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
109             405             410             415
110      aaa tag      1254
111      Lys
113 <210> SEQ ID NO: 2
114 <211> LENGTH: 417
115 <212> TYPE: PRT
116 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: artificial peptide sequence based on human
119      sequence
120 <400> SEQUENCE: 2
121      Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys
122      1             5             10             15
123      Lys Ser Ser Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu
124             20             25             30
125      Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Lys Ile Ser
126             35             40             45
127      Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
128             50             55             60
129      Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
130      65             70             75             80
131      Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
132             85             90             95
133      Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
134             100            105            110
135      Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
136             115            120            125
137      Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
138             130            135            140
139      Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
140      145            150            155            160
141      Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
142             165            170            175
143      Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu Glu Ser Lys Tyr
144             180            185            190
145      Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
146             195            200            205
147      Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser

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148          210          215          220
149  Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
150  225          230          235          240
151  Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
152          245          250          255
153  Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
154          260          265          270
155  Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
156          275          280          285
157  Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
158          290          295          300
159  Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
160          305          310          315          320
161  Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
162          325          330          335
163  Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
164          340          345          350
165  Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
166          355          360          365
167  Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
168          370          375          380
169  Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
170          385          390          395          400
171  Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
172          405          410          415
173  Lys
175 <210> SEQ ID NO: 3
176 <211> LENGTH: 2
177 <212> TYPE: PRT
178 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: artificial peptide linker sequence
181 <400> SEQUENCE: 3
182  Gly Ser
183  1
185 <210> SEQ ID NO: 4
186 <211> LENGTH: 7
187 <212> TYPE: PRT
188 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: artificial peptide linker sequence
191 <400> SEQUENCE: 4
192  Gly Gly Ser Gly Gly Gly Ser
193  1 5
195 <210> SEQ ID NO: 5
196 <211> LENGTH: 12
197 <212> TYPE: PRT
198 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:

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200 <223> OTHER INFORMATION: artificial peptide linker sequence
 201 <400> SEQUENCE: 5
 202 Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 203 1 5 10
 205 <210> SEQ ID NO: 6
 206 <211> LENGTH: 17
 207 <212> TYPE: PRT
 208 <213> ORGANISM: Artificial Sequence
 209 <220> FEATURE:
 210 <223> OTHER INFORMATION: artificial peptide linker sequence
 211 <400> SEQUENCE: 6
 212 Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 213 1 5 10 15
 214 Ser
 216 <210> SEQ ID NO: 7
 217 <211> LENGTH: 23
 218 <212> TYPE: PRT
 219 <213> ORGANISM: Artificial Sequence
 220 <220> FEATURE:
 221 <223> OTHER INFORMATION: artificial peptide linker sequence
 222 <400> SEQUENCE: 7
 223 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 224 1 5 10 15
 225 Gly Ser Gly Gly Gly Ser
 226 20
 228 <210> SEQ ID NO: 8
 229 <211> LENGTH: 30
 230 <212> TYPE: PRT
 231 <213> ORGANISM: Artificial Sequence
 232 <220> FEATURE:
 233 <223> OTHER INFORMATION: artificial peptide linker sequence
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 235 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly
 236 1 5 10 15
 237 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 238 20 25 30
 240 <210> SEQ ID NO: 9
 241 <211> LENGTH: 40
 242 <212> TYPE: PRT
 243 <213> ORGANISM: artificial sequence
 244 <220> FEATURE:
 245 <223> OTHER INFORMATION: artificial peptide linker sequence
 246 <400> SEQUENCE: 9
 247 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly
 248 1 5 10 15
 249 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 250 20 25 30
 251 Gly Gly Ser Gly Gly Gly Gly Ser
 252 35 40

VERIFICATION SUMMARY

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